

55440T0"080522550

5'	NAG	GAN	GGT	GGG	GGA	CCC	ANG	GGT	CCA	GAG	CGC	AGT	TCG	GGT	CGG	AGC	TYC	GWC
			63			72			81			90			99			108
	CAG	GCT	GCT	GGT	ACC	TGC	GTC	CGC	CCG	GCG	AGC	AGG	ACA	GGC	TGC	TTT	GGT	TTG
			117			126			135			144			153			162
	TGA	CCT	CCA	GGC	AGG	ACG	GCC	ATC	CTC	TCC	AGA	ATG	AAG	ATC	TTC	TTG	CCA	GTG
												M	K	I	F	L	P	V
			171			180			189			198			207			216
	CTG	CTG	GCT	GCC	CTT	CTG	GGT	GTG	GAG	CGA	GCC	AGC	TCG	CTG	ATG	TGC	TTT	TCC
	L	L	A	A	L	L	G	V	E	R	A	S	S	L	M	C	F	S
			225			234			243			252			261			270
	TGC	TTG	AAC	CAG	AAG	AGC	AAT	CTG	TAC	TGC	CTG	AAG	CCG	ACC	ATC	TGC	TCC	GAC
	C	L	N	Q	K	S	N	L	Y	C	L	K	P	T	I	C	S	D
			279			288			297			306			315			324
	CAG	GAC	AAC	TAC	TGC	GTG	ACT	GTG	TCT	GCT	AGT	GCC	GGC	ATT	GGG	AAT	CTC	GTG
	Q	D	N	Y	C	V	T	V	S	A	S	A	G	I	G	N	L	V
			333			342			351			360			369			378
	ACA	TTT	GGC	CAC	AGC	CTG	AGC	AAG	ACC	TGT	TCC	CCG	GCC	TGC	CCC	ATC	CCA	GAA
	T	F	G	H	S	L	S	K	T	C	S	P	A	C	P	I	P	E
			387			396			405			414			423			432
	GGC	GTC	AAT	GTT	GGT	GTG	GCT	TCC	ATG	GGC	ATC	AGC	TGC	TGC	CAG	AGC	TTT	CTG
	G	V	N	V	G	V	A	S	M	G	I	S	C	C	Q	S	F	L
			441			450			459			468			477			486
	TGC	AAT	TTC	AGT	GCG	GCC	GAT	GGC	GGG	CTG	CGG	GCA	AGC	GTC	ACC	CTG	CTG	GGT
	C	N	F	S	A	A	D	G	G	L	R	A	S	V	T	L	L	G
			495			504			513			522			531			
	GCC	GGG	CTG	CTG	CTG	AGC	CTG	WTG	CCG	GCC	CTG	CTG	CGG	TTT	GGC	CCC	TGA	3'
	A	G	L	L	L	S	L	(X)	P	A	L	L	R	F	G	P	*	

7
25
43
61
79
97
115
128

FIGURE 1

1	M	-	-	-	-	K	I	F	L	P	V	L	L	A	A	L	L	G	V	E	R	A	S	S	L	M	C	F	scah-1		
1	M	S	A	T	S	N	M	R	V	F	L	P	V	L	L	A	A	L	L	G	M	E	Q	V	H	S	L	M	C	F	GI 434660
1	M	S	T	T	S	S	M	R	V	F	S	I	V	L	Q	A	H	L	L	G	V	E	L	V	P	S	L	I	C	S	GI 1199651
1	M	-	-	-	-	-	K	A	V	L	L	A	L	L	M	A	G	L	A	L	Q	P	G	T	A	L	L	C	Y	scah-2	
1	M	-	-	-	-	-	K	A	F	L	F	A	V	L	A	A	V	L	C	V	E	R	A	H	T	L	I	C	F	GI 509840	
25	S	C	L	N	Q	K	S	N	L	Y	C	L	K	P	T	I	C	S	D	Q	D	N	Y	C	V	T	V	S	A	S	scah-1
31	S	C	T	D	Q	K	N	N	I	N	C	L	W	P	V	S	C	Q	E	K	D	H	Y	C	I	T	L	S	A	A	GI 434660
31	S	C	T	H	Q	K	S	N	I	N	P	P	W	P	V	A	C	K	D	T	G	N	Y	C	I	M	L	F	S	A	GI 1199651
25	S	C	K	A	Q	V	S	N	E	D	C	L	Q	V	E	N	C	T	Q	L	G	E	Q	C	W	T	A	R	I	R	scah-2
25	S	C	S	D	A	S	S	N	W	A	C	L	T	P	V	K	C	A	E	N	E	E	H	C	V	T	T	Y	V	G	GI 509840
55	A	G	I	G	N	L	V	T	F	G	H	S	L	S	K	T	C	S	P	A	C	P	I	P	E	-	G	V	N	V	scah-1
61	A	G	F	G	N	-	V	N	L	G	Y	T	L	N	K	G	C	S	P	I	C	P	S	E	N	V	N	L	N	L	GI 434660
61	V	G	F	G	N	-	V	N	L	G	Y	T	L	N	T	G	C	S	Q	S	C	P	H	E	N	I	N	I	N	P	GI 1199651
55	A	V	-	-	G	L	L	T	V	-	-	I	S	K	G	C	S	L	N	C	V	D	D	S	Q	D	Y	Y	V	scah-2	
55	V	G	I	G	G	-	-	K	S	G	Q	S	I	S	K	G	C	S	P	V	C	P	S	A	G	I	N	L	-	-	GI 509840
84	G	V	A	S	M	G	I	S	C	C	Q	S	F	L	C	N	F	S	A	A	D	G	G	L	R	A	S	V	T	L	scah-1
90	G	V	A	S	V	N	S	Y	C	C	Q	S	S	F	C	N	F	S	A	A	G	L	G	L	R	A	S	I	P	L	GI 434660
90	G	V	A	S	V	N	S	Y	-	-	Q	S	S	F	C	N	F	S	N	A	C	L								GI 1199651	
80	G	K	K	N	I	T	-	-	C	C	D	T	D	L	C	N	X	S	G	A	H	-	A	L	Q	P	A	A	A	I	scah-2
81	G	I	A	A	A	S	V	Y	C	C	D	S	F	L	C	N	I	S	G	S	S	-	S	V							

Decoration 'Decoration #1': Box residues that match the Consensus exactly.

FIGURE 3

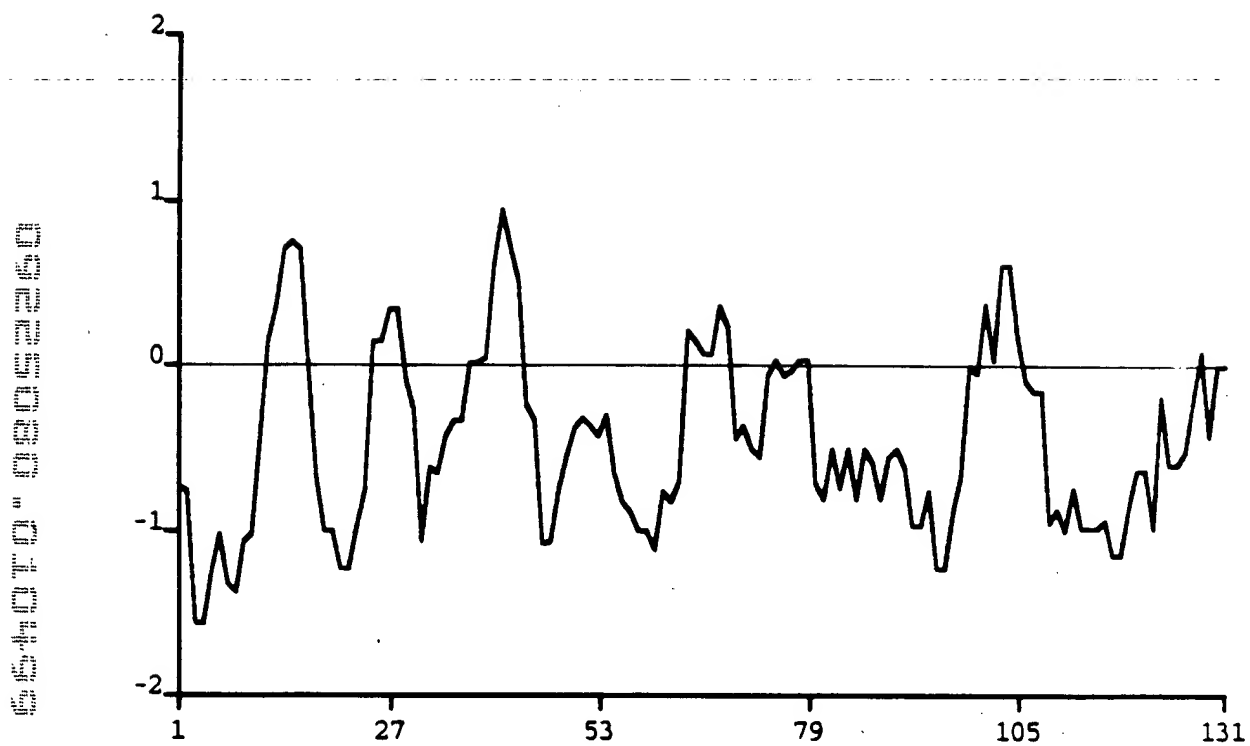


FIGURE 4

054010-030540

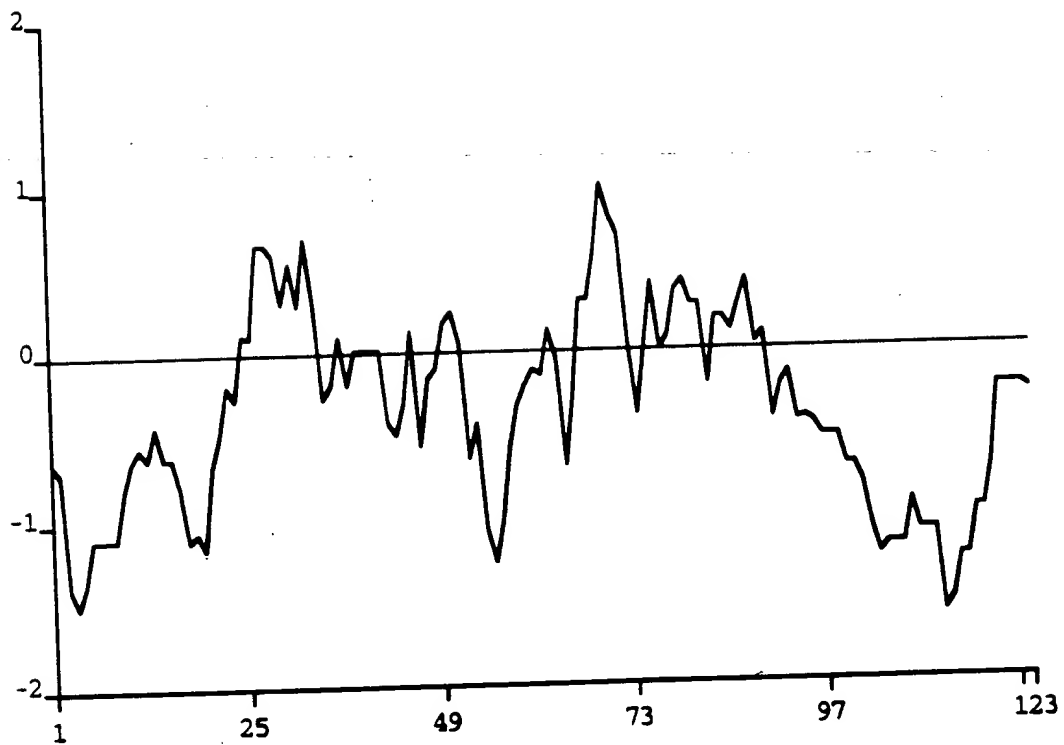
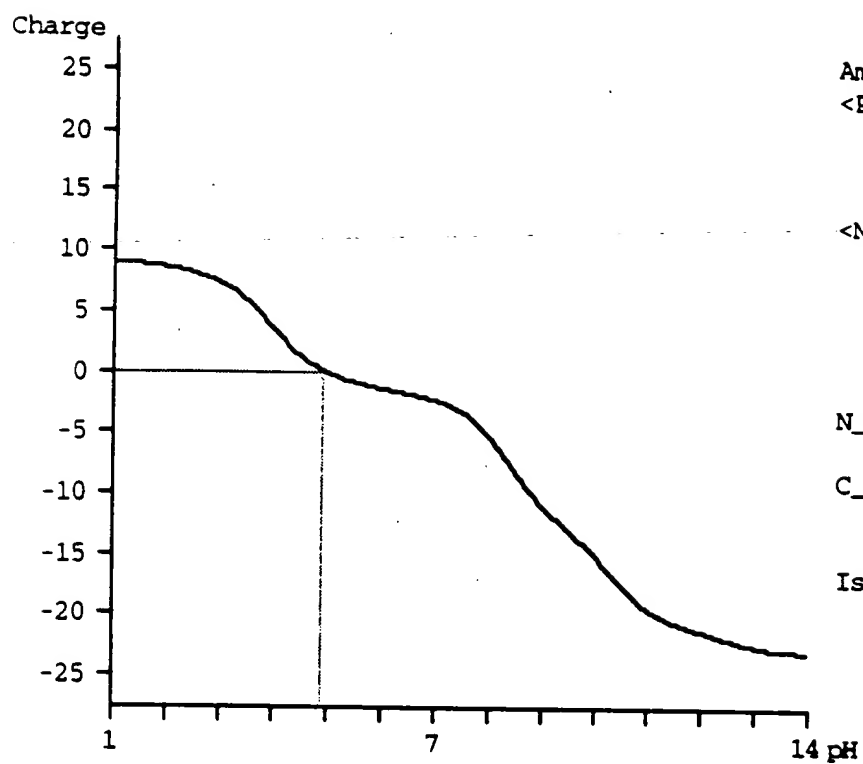


FIGURE 5



Amino Acid	Number	pKa
<Positive>		
Arg(R)	2	12.5
His(H)	1	6.0
Lys(K)	5	10.5
<Negative>		
Asp(D)	6	3.9
Cys(C)	10	8.3
Glu(E)	3	4.3
Tyr(Y)	3	10.1
N_terminal	Met(M)	9.3
C_terminal	Leu(L)	2.3
Isoelectric point [pI]		4.93

FIGURE 7